wCorr Arguments

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This vignette explores two Boolean switches in the package. First, the ML switch allows for either a non-MLE (but consistent) esitimate of the nusiance parameters that define the binning process to be used (ML=FALSE) or for the nusiance parameters to be estimated using the MLE (ML=TRUE). Second the fast argument gives the option to use a pure R implementation (fast=FALSE) or an implementation that relies on the Rcpp and RcppArmadillo packages (fast=TRUE).

Numerical simulations show that the results are essentially unaffected by either of these switches and so it is recomended to use fast=TRUE and ML=FALSE which will drastically speed computation.

The "wCorr Formulas" vignette describes the statistical properties of the correlation estimators in the package.

ML switch

The correlation coefficients between two vectors of random variables that are jointly bivariate normal–call the vectors X and Y.

$$\begin{pmatrix} X \\ Y \end{pmatrix} \sim N \left[\begin{pmatrix} \mu_x \\ \mu_y \end{pmatrix}, \Sigma \right]$$

where $N(\mathbf{A}, \mathbf{\Sigma})$ is the bivariate normal distribution with mean \mathbf{A} and covariance $\mathbf{\Sigma}$.

The i^{th} members of the vectors are then called x_i and y_i .

Polyserial computation

The derivatives of ℓ can be computed but are not readily computed and so when the ML argumet is set to FALSE (the default) a one dimensional optimization of ρ is calculated using stats::optimize. When the ML argument is set to TRUE a multi-dimensional optimization is done for ρ and θ using minqa::bobyqa. As is shown below, the difference between these two is slight, if present, and so the default value of ML is recomended.

Because the optimization is not perfect when the correlation is in a boundary condition ($\rho \in \{-1,1\}$), a check for perfect correlation is performed before the above optimization by simply seeing if the values of X and M have exactly the same order.

Polychoric computation

This again mirrors the treatment of the polyserial. The derivatives of ℓ can be computed but are not readily computed and so when the ML argumet is set to FALSE (the default) a one dimensional optimization of ρ is calculated using stats::optimize. When the ML argument is set to TRUE a multi-dimensional optimization is done for ρ , θ , and θ' using minqa::bobyqa. As is shown below, the difference between these two is slight, if present, and so the default value of ML is recomended.

Because the optimization is not perfect when the correlation is in a boundary condition ($\rho \in \{-1, 1\}$), a check for perfect correlation is performed before the above optimization by simply seeing if the values of P and M have a Goodman-Kruskal correlation coefficient of -1 or 1. When this is the case, the MLE of -1 or 1, respectively, is returned.

General setup for the unweighted case

A simulation is run several times using the following method:

- selecting a value of n (the number of observations)
- selecting a true correlation coefficient ρ
- generating X and Y
- selecting the value of t and t' (the number of bins for M and P)
- selecting $\boldsymbol{\theta}$ and $\boldsymbol{\theta}'$
- confirming that at least 2 levels of M and P are occupied (if not, retrun to generating X and Y)
- calculating and recording relevant statistics

ML switch

It is easy to prove the consistency of the θ for the polyserial and θ and θ' using the non-ML case. Similarly, for ρ , because it is an MLE that can be obtained by taking a derivative and setting it equal to zero, the results are asymptotically unbiased and obtain the Cramer-Rao lower bound.

This does not speak to the small sample properties of these correlation coefficients. Previous work has described their properties by simulation and so that tradition is continued below.

• plot that shows difference as a function of ρ and at n=10 and n=1000000 between ML=FALSE and ML=TRUE when fast=TRUE

fast switch

This section looks at the agreement between the pure R implementation of the optimizations and the Rcpp and RcppArmadillo impelementation. The code can compute with either option by setting fast=FALSE (pure R) or fast=TRUE (Rcpp).

This is the summary of all differences between the fast=TRUE and fast=FALSE runs for the polyserial

- plot that shows difference as a function of ρ and at n=10 and n=1000000 between fast=FALSE and fast=TRUE when ML=TRUE
- plot that shows difference as a function of ρ and at n=10 and n=10000 between fast=FALSE and fast=TRUE when ML=FALSE

Implications for speed

• plot of compute time vs n for all four options. Each stop when the mean >= 20 seconds